

FIG. 1A

TCGATAGGTA	CCCACTATAG	GGCACGCGTG	GTCGACGGCC	CGGGCTGGTC	50
1					
TGGCAACTTC	AAGTG TGGG	CTTTCAGACC	GGCATCATCA	GTGTTACGGG	100
51					
GAAGTCACTA	GGAATGCAGA	ATTGATTGAG	CACGGTGGCT	CACACCTGTA	150
101					
ATCCCAACAC	TCTGGGAGGC	CAAGGCAGGT	GGATCACTTG	TGGTCAGGAG	200
151					
TTTGAGACCA	GCCTGGCCAA	CATGGTGAAA	CCTCATCTCT	ACTAAAAATA	250
201					
CAAAAATTAG	CTGGGAATGG	TGGCACATGC	CTATAATCCC	AGTTACTCAG	300
251					
GAGGCTGAGG	CAGGAGAATC	ATTTGAACCT	GGGAGGCAGA	GGTTGCAGTG	350
301					
AGCCGAGATC	ACGCCACTGC	ACTCCAGCCT	GGGTGACACA	GCGAGACTCT	400
351					
GTCTCAAAAA	AAAAAAATG	CAGAATTTCA	GGCTTCACCC	CAGACCCACT	450
401					
GCATGACTGC	ATGAGAAGCT	GCATCTTAAC	AAGATCCCTG	GTAATTCATA	500
451					
CGCATATTAA	ATTTGGAGAT	GCACTGGCGT	AAGACCCTCC	TACTCTCTGC	550
501					
TTAGGCCCAT	GAGTTCTTCC	TTTACTGTCA	TTCTCCACTC	ACCCCAAAC	600
551					
TTGAGCCTAC	CCTTCCCACC	TTGGCGGTAA	GGACACAACC	TCCCTCACAT	650
601					
TCCTACCAGG	ACCCTAAGCT	TCCCTGGGAC	TGAGGAAGAT	AGAATAGTTC	700
651					
GTGGAGCAAA	CAGATATACA	GCAACAGTCT	CTGTACAGCT	CTCAGGCTTC	750
701					

00014000-034104



**FIG. 1B**

[illegible]

FIG. 1C

ATTCTCAGTC 1501	CAACAAATGG	TTGCTGCCCA	AGGCTGACTG	TGCCCCACCC 1550
CAACCCCTGC 1551	TGGCCAGGGT	CAATGTCTGT	CTCTCTGGTC	TCTCCAGAAG 1600
TCTTCCATGG 1601	CCACCTTCGT	CCCCACCCTC	CAGAGGAATC	TGAAACCGCA 1650
TGTGCTCCCT 1651	GGCCCCCACA	GCCCCTGCCT	CTCCAGAGC	AGCAGTACCT 1700
AAGCCTCAGT 1701	GCACTCCAAG	AATTGAAACC	CTCAGTCTGC	TGCCCCCTCCC 1750
CACCAGAATG 1751	TTTCTCTCCC	ATTCTTACCC	ACTCAAGGCC	CTTTCAGTAG 1800
CCCCTTGGAG 1801	TATTCTCTTC	CTACATATCA	GGGCAACTTC	CAAACCTCATC 1850
ACCCTTCTGA 1851	GGGGTGGGGG	AAAGACCCCC	ACCACATCGG	GGGAGCAGTC 1900
CTCCAAGGAC 1901	TGGCCAGTCT	CCAGATGCCC	GTGCACACAG	GAACACTGCC 1950
TTATGCACGG 1951	GAGTCCCAGA	AGAAGGGGTG	ATTTCTTTCC	CCACCTTAGT 2000
TACACCATCA 2001	AGACCCAGCC	AGGGCATCCC	CCCTCCTGGC	CTGAGGGCCA 2050
GCTCCCCATC 2051	CTGAAAAACC	TGTCTGCTCT	CCCCACCCTT	TTGAGGCTAT 2100
AGGGCCCAAG 2101	GGGCAGGTTG	GACTGGATTC	CCCTCCAGCC	CCTCCCGCCC 2150
CCAGGACAAA 2151	ATCAGCCACC	CCAGGGGCAG	GGCCTCACTT	GCCTCAGGAA 2200
CCCCAGCCTG 2201	CCAGCACCTA	TTCCACCTCC	CAGCCCAGCA 2239	



FIG. 2A

CTCGAGGATCTCGGCCCTCTTTCTGCATCCTTGTCCTAAATCATTTTCAT  
1 50  
ATCTTGCTAGACCTCAGTTTGAGAGAAACGAACCTTCTCATTTTCAAGTT  
51 100  
GAAAAAAAAAGAGGTTCAAAGTGGCTCACTCAAAGTTACAAGCCAACAC  
101 150  
TCACCACTACGAGTACAATGGCCACCATTAGTGCTGGCATGCCCCAGGAG  
151 200  
ACAGGCATGCATATTATTCTAGATGACTGGGAGGCAGAGGGGTGGCCTAG  
201 250  
TGAGGTCAGACTGTGGACAGATCAGGCAGATGTGGGTTCTGATCCCAATT  
251 300  
CCTCAGGCCGCAGAACTACTGTGGTTCAAGAAGGGGACAAAAGGACTGCA  
301 350  
GTCCGGAACAGGAGGTCCATTTGAGAGCTGACTGAGCAGAAGAGGAAAGT  
351 400  
GAAGAACTTCTGGGGCAAGAGCTTACCCTACTTTACAGCTTGTGTCTT  
401 450  
CTTTACTCCAGGGGCGTCCCTGGTACTCAGTAAATGTCTGTTGGCTTGAG  
451 500  
GAACATATGTGTAAGGAGGAAGGAGAGGGAAGTCTGAGGGAGTTAAGACTC  
501 550  
AAGAATCAATCAAGGAGAGGACAGCAGAGAAGACAGGGTTTGGGAGAGAG  
551 600  
ACTCCAGACATTGGCCCTGGTTCCCTTCTTGGCCACTGTGAAACCTCCA  
601 650  
GAGGAACTGAGTGCTGTGGCTTTAAATGATCTCAGCACTGTCAGTGAAGC  
651 700  
GCTCTGCTCAAAGAGTTATCCTCTTGCTCCTGTGCCGGGGCCTCCCCCTC  
701 750  
CTCTCAGCTCCCAAACCTTCTCAGCCACTGTGATGGCATAATTAGATGC  
751 800  
GAGAGCTCAGACCGTCAGGTCTGCTCCAGGAACCACCATTTTCCCCAAC  
801 850

004400-2027860



FIG. 2B

CCCAGAGAAAGGTCCTAGTGGAAGTGGGGGCCACTGAAGGGCTGATGG 900  
851  
GGTTCTGTCCTTTCCCCCATGCTGGGTGGACTTAAAGTCTGCGATGTGTG 950  
900  
TAGGGGGTAGAAGACAACAGAACCTGGGGGCTCCGGCTGGGAGCAGGAGG 1000  
951  
AACTCTCACCAGACGATCTCCAAATTTACTGTGCAATGGACGATCAGGAA 1050  
1001  
ACTGGTTCAGATGTAGCTTCTGATACAGTGGGTCTGAGGTAAAACCCGAA 1100  
1051  
ACTTAATTTCTTTCAAAAATTTAAAGTTGCATTTATTATTTTATATGTGT 1150  
1101  
GCCCATATGTGTGCCACAGTGTCTATGTGGAGGTCAGAGGGCAAGTTGTG 1200  
1151  
GGCATTGGCTCTCTCCTTTTATAATGTGGCTTCTGGGGACCAAATGTCA 1250  
1201  
GGCATGGTGGCAAGAGCTTTTACCTGTTGAGCCATCTCATGGTTTCGTAA 1300  
1251  
AACTTCCTATGACGCTTACAGGTAACGCAGAGACACAGACTCACATTTGG 1350  
1301  
AGTTAGCAGATGCTGTATTGGTGTAACACTCATAACAGACACACACAC 1400  
1351  
ATACTCATAACACACACACACTTATCATATGCACACACATACTCGTA 1450  
1401  
TACACACAGACACACACATGCACTCTCACATTACATATTCATACACA 1500  
1451  
TCCACACACACTCATCCACACACAGACACACATACTCATCCACACA 1550  
1501  
CACACACACATACTCATAACACACACAGACACACATACTCATAACA 1600  
1551  
CACACAGACACACATATAATCATAACACAGACACACTCATACATG 1650  
1601  
TGCACACACACTCATCCACACACACACTCATAACACACACACTCA 1700  
1651

404220-2247300

FIG: 2C

TACACACACACTCATACACACACACGAGGTTTTCTCAGGCTGCCT  
1701 1750

TTGGGTGGAGACTGGAAGTCTGTTTTTCAGCTCCTTGGCTTTTTG  
1751 1800

TCCCTTTAGATGAGATCTCCTCCTCACTTTACACACAGAAAGATCACACA  
1801 1850

CGAGGGAGAACTGGCGGTGCGGAAGAGGGCTACACGGTAGGGTGTGAGG  
1851 1900

TCAGGAGATCTTCTGGCAAGTCTCAAACCTCCACATAGCACAGTGTTTA  
1901 1950

CGTGAGGATTTAGGAGGAATCAGGAAGAGGATTGGTTTACTGCAGAGCAG  
1951 2000

ACCATATAGGTCCACTCCTAAGCCCCATTTGAAATTAGAAGTGAGACAGT  
2001 2050

GTGGGATAAAAAGAGCAGATCTCTGGTCACATTTTAAAGGGATATGAGG  
2051 3000

GTCCTGTGCCTTTAAGCCTTCCCATCTCCCTCCAATCCCCCCTCACCTTC  
2101 2150

CCCACCCTAACCTCCCCAGGTTTCTGGAGGAGCAGAGTTGCGTCTTCTC  
2151 2200

CCTGCCCTGCCGAGCTGCTCACTGGCTGCTCTAGAGGCTGTGCTTTGCGG  
2201 2250

TCTCCATGGAACCATTAGTTGCTAAGCAACTGGAGCATCATCTGTGCTG  
2251 2300

AGCTCAGGTCCTATCGAGTTCACCTAGCTGAGACACCCACGCCCCTGCAG  
2301 2350

CCACTTTGCAGTGACAAGCCTGAGTCTCAGGTTCTGCATCTATAAAAACG  
2351 2400

AGTAGCCTTTTCAAGAGGGCATGCAGAGCCCCCTGGCCAGCGTCTAGAGGA  
2401 2450

GAGGTGACTGAGTGGGGCCATGTCACTCGTCCATGGCTGGAGAACCTCCA  
2451 2500

TCAGTCTCCCAGTTAGCCTGGGGCAGGAGAGAACCAGAGGAGCTGTGGCT  
2501 2550

00014202-03010

FIG. 2D

GCTGATTGGATGATTACGTACCCAATCTGTTGTCCAGGCATCGAACCC  
2551 2600

CAGAGCGACCTGCACACATGCCACCGCTGCCCCGCCCTCCACCTCCTCTG  
2601 2650

CTCCTGGTTACAGGATTGTTTTGTCTTGAAGGGTTTTGTTGTGCTACTT  
2651 2700

TTTGCTTGTTTTTCTTTTTTAACATAAGGTTTCTCTGTGTAGCCCTAG  
2701 2750

CTGTCTGGAACTCACTCTGTAGACCAGGCTGGCCTCAAACCTCAGAAATC  
2751 2800

CACCTTCCTCCCAAGTGCTGGGATTAAAGGCATTGACCATCGCCCAGC  
2801 2850

CCCCGGTCTTGTTTCCTAAGGTTTTCTGCTTTACTCGCTACCCGTTGCA  
2851 2900

CAACCGCTTGCTGTCCAAGTCTGTTTGTATCTACTCCACCGCCCACTAGC  
2901 2950

CTTGCTGGACTGGACCTACGTTTACCTGGAAGCCTTCACTAACTTCCCTT  
2951 3000

GTCTCCACCTTCTGGAGAAATCTGAAGGCTCACACTGATACCCTCCGCTT  
3001 3050

CTCCCAGAGTCGCAGTTTCTTAGGCCTCAGTTAAATACCAGAATTGGATC  
3051 3100

TCAGGCTCTGCTATCCCCACCCTACCTAACCAACCCCTCCTCTCCCATC  
3101 3150

CTTACTAGCCAAAGCCCTTCAACCCTTGGGGCTTTTCTACACCTACAC  
3151 3200

ACCAGGGCAATTTTAGAACTCATGGCTCTCCTAGAAAACGCCTACCTCCT  
3201 3250

TGGAGACTGACCCTCTACAGTCCAGGAGGCAGACACTCAGACAGAGGAAC  
3251 3300

TCTGTCCTTCAGTCGCGGGAGTTCCAGAAAGAGCCATACTCCCCTGCAGA  
3301 3350

GCTAACTAAGCTGCCAGGACCCAGCCAGAGCATCCCCCTTTAGCCGAGGG  
3351 3400

004422-0224360



FIG. 2E

CCAGCTCCCAGAATGAAAAACCTGTCTGGGGCCCCTCCCTGAGGCTACA 3450

GTCGCCAAGGGGCAAGTTGGACTGGATTCCCAGCAGCCCCTCCCACTCCG 3500

AGACAAAATCAGCTACCCTGGGGCAGGCCTCATTGGCCCCAGGAAACCCC 3550

AGCCTGTCAGCACCTGTTCCAGGATCCAGTCCCAGCGCAGTA 3592

CCCTGAGGCTACA



Figure 3A

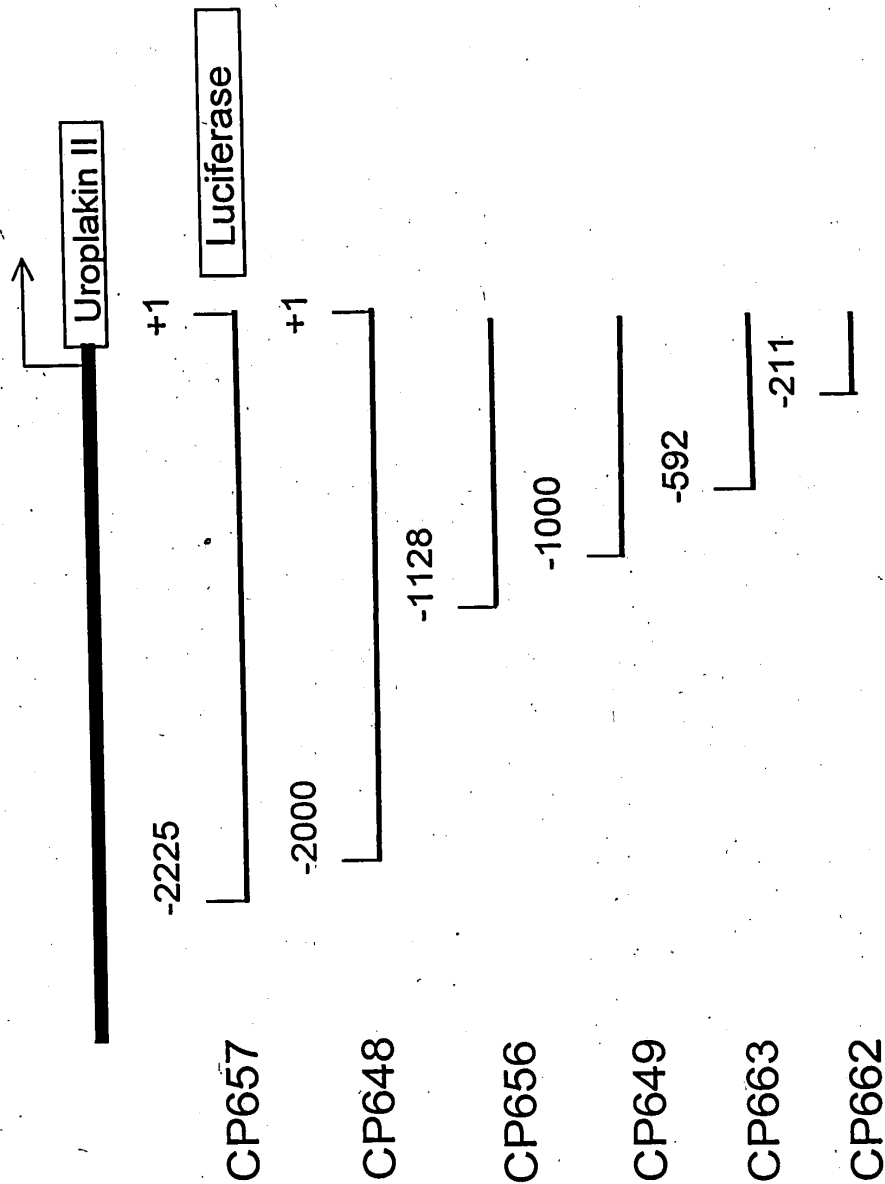


Figure 3B

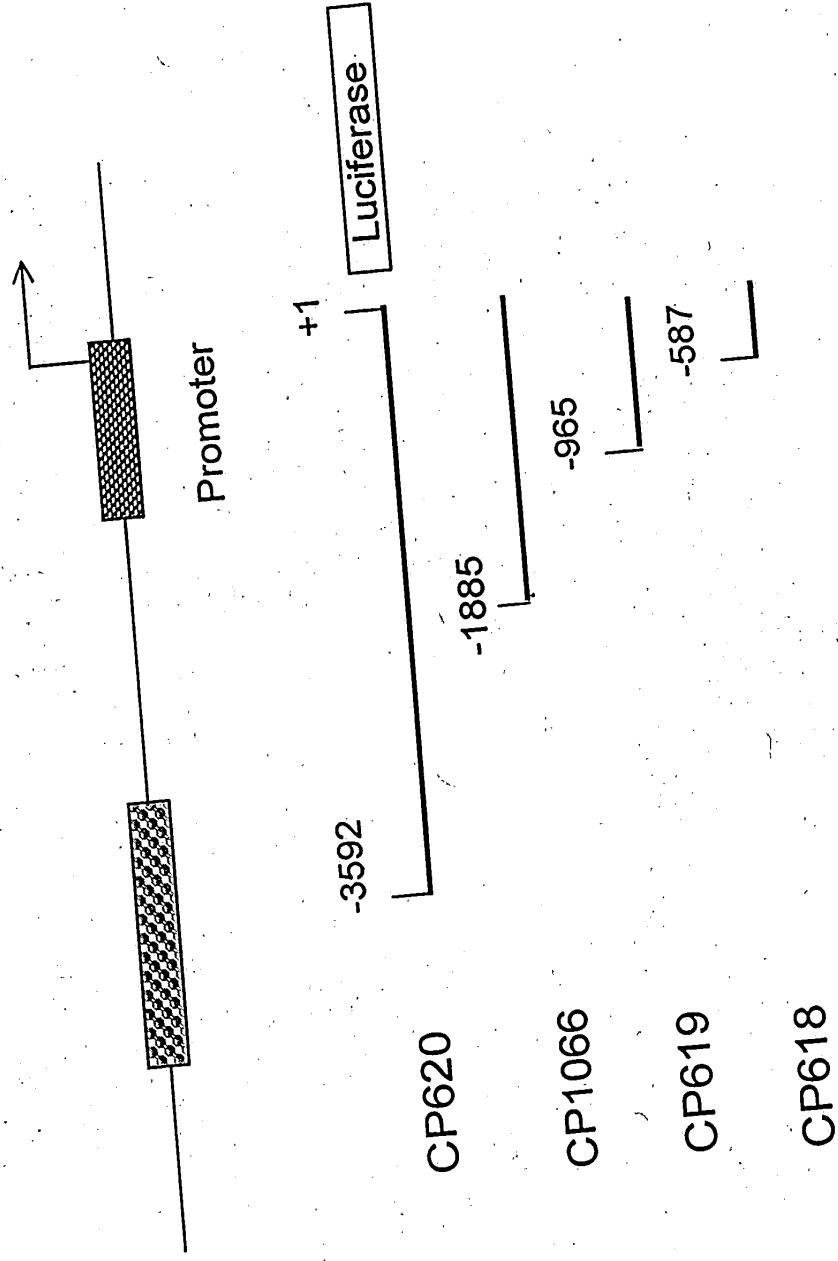


Figure 4A

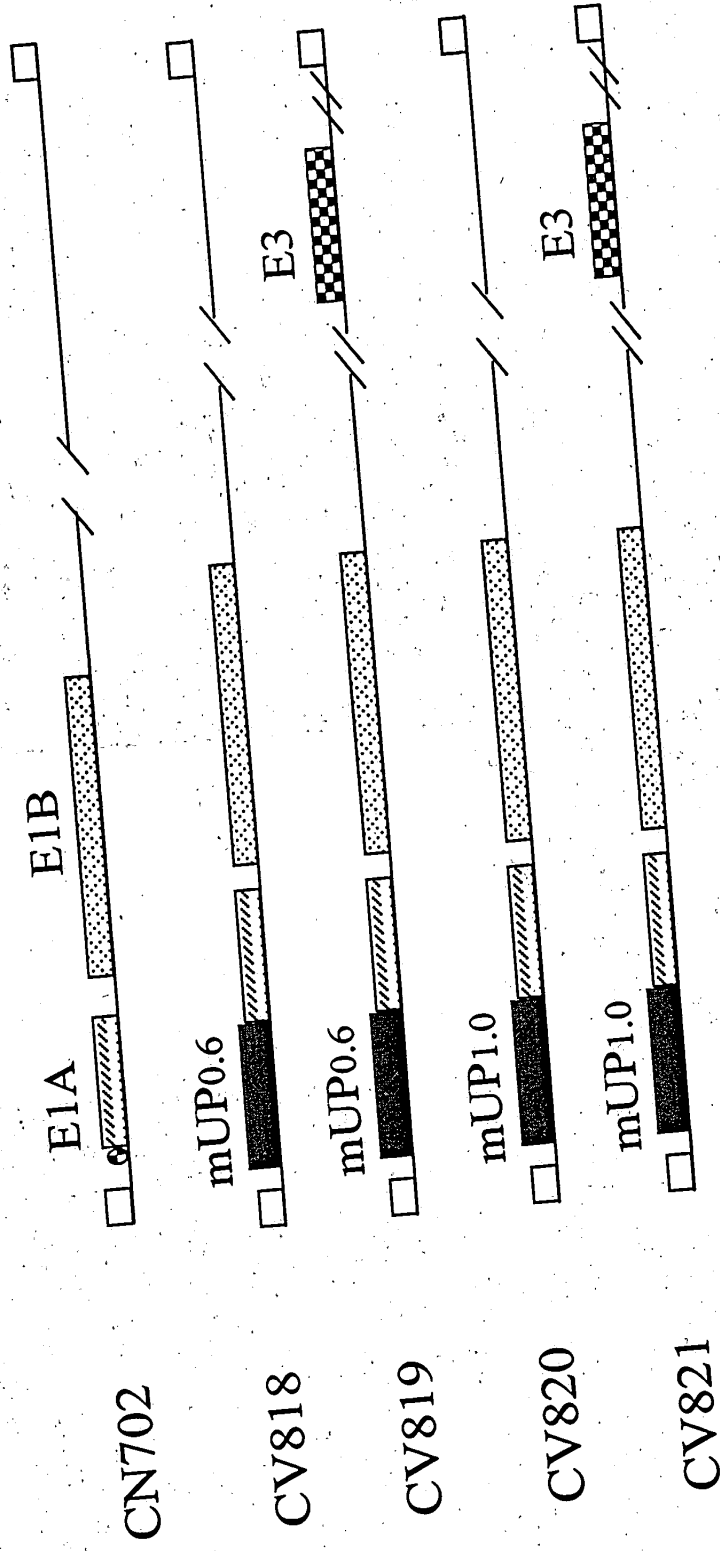


Figure 4B

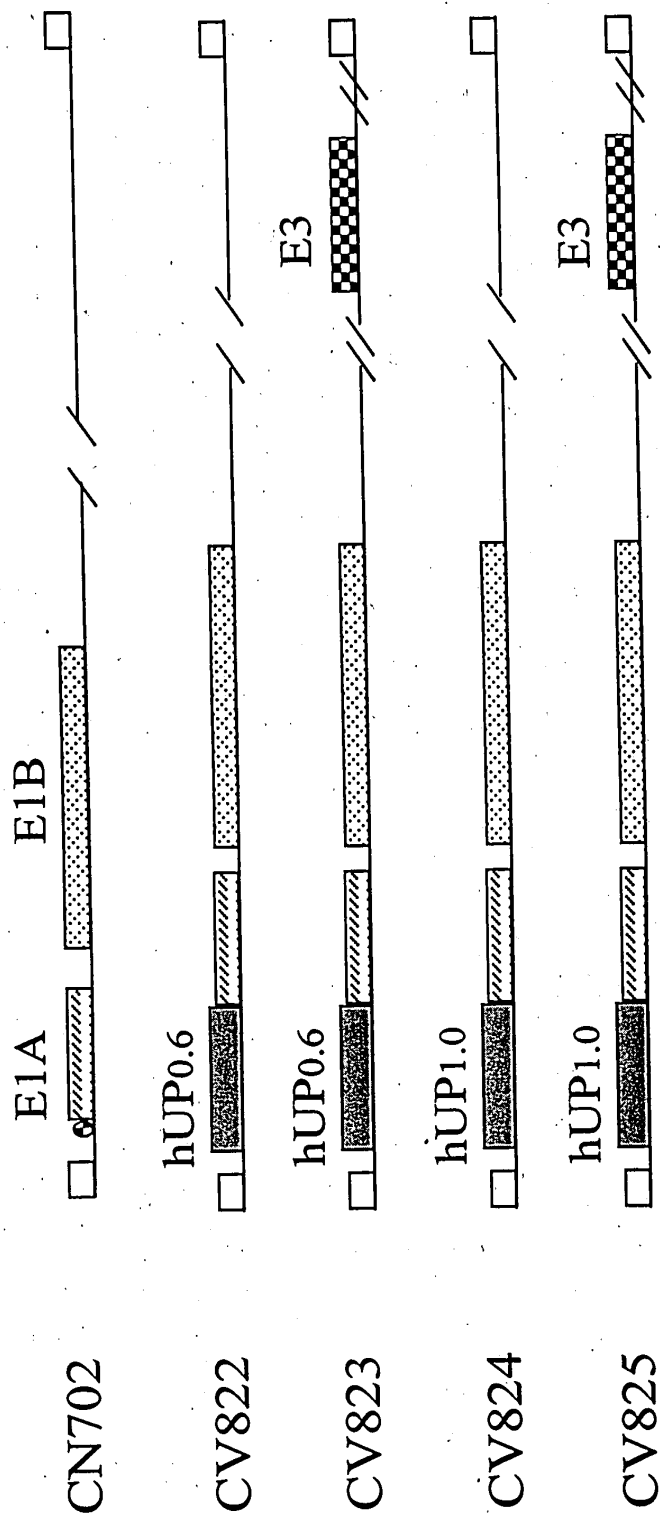


Figure 4C

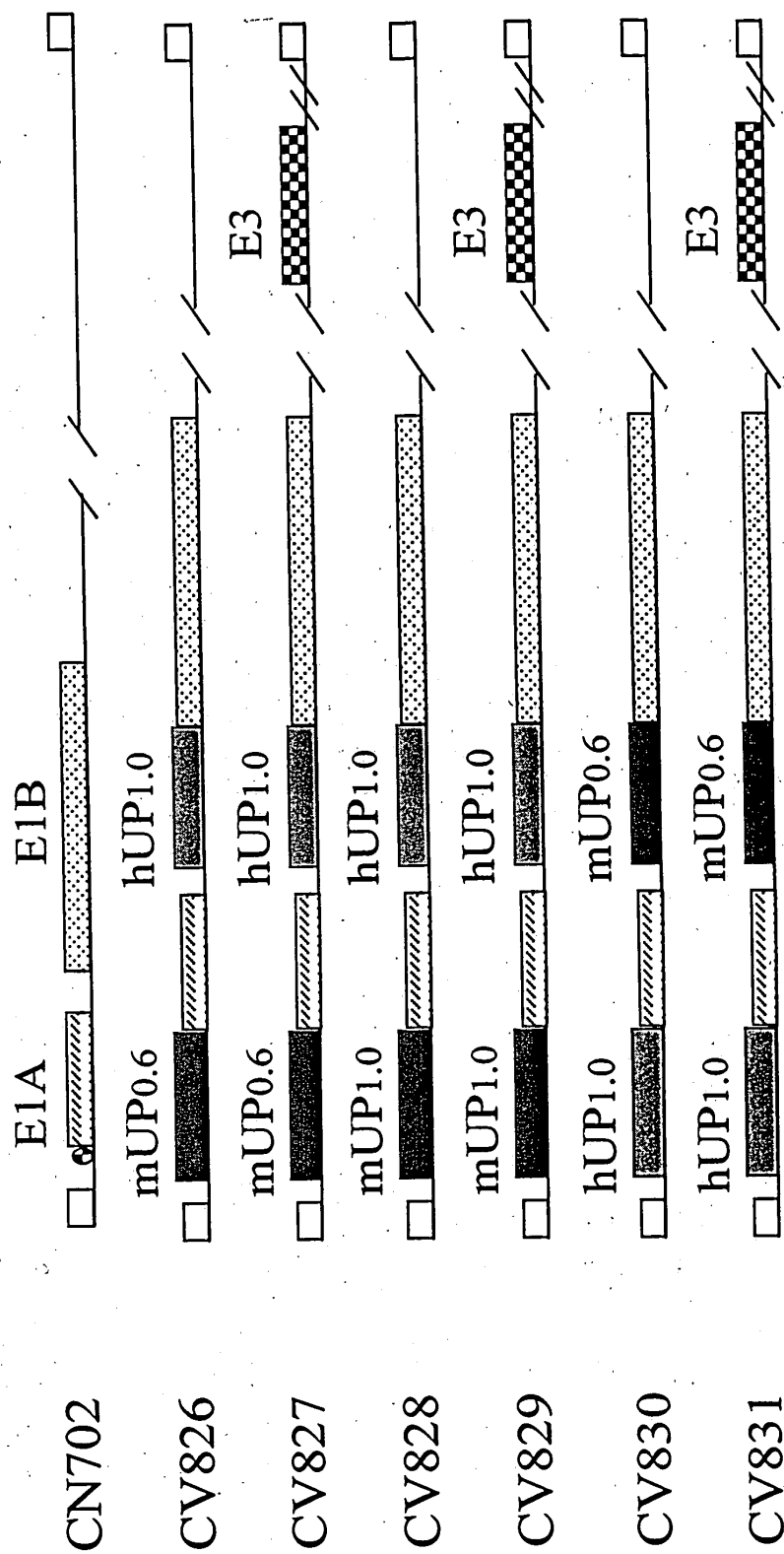
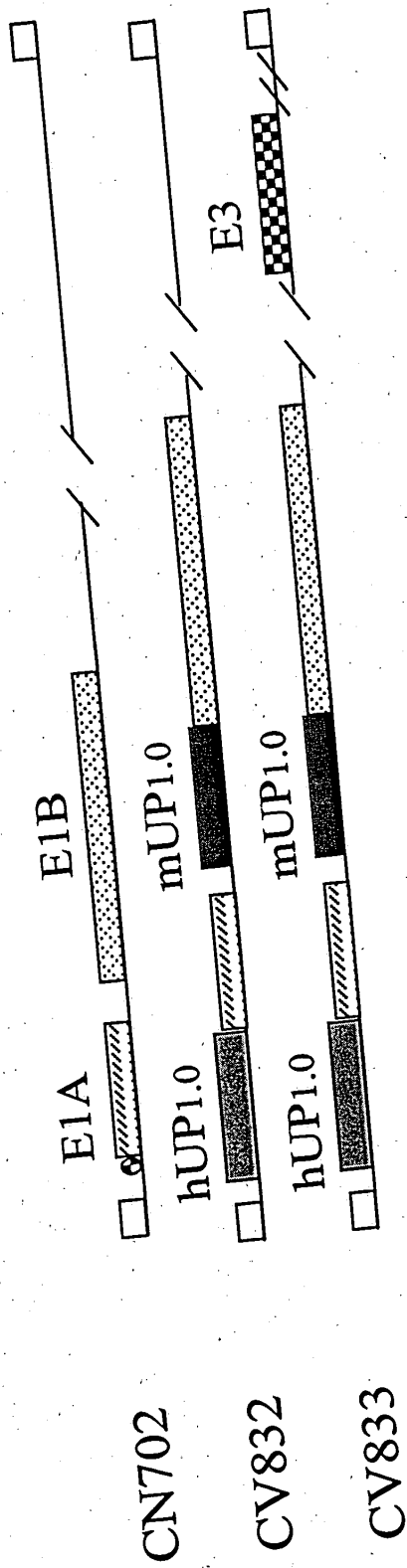


Figure 4D



FOUO-2021BDD

Figure 4E

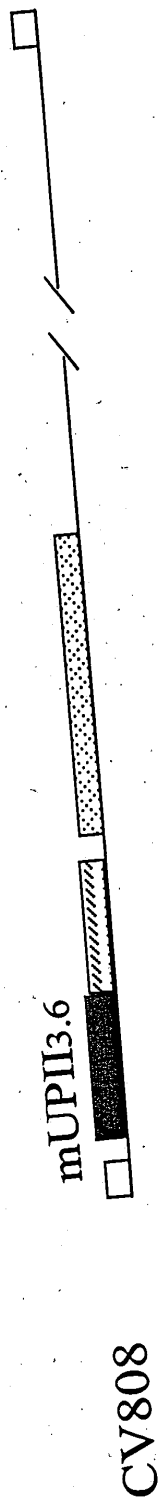
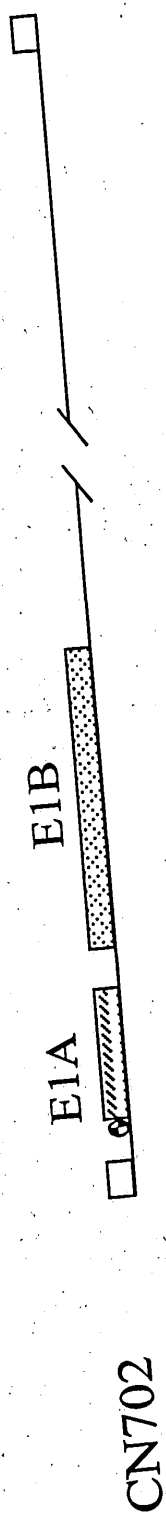


Figure 4F

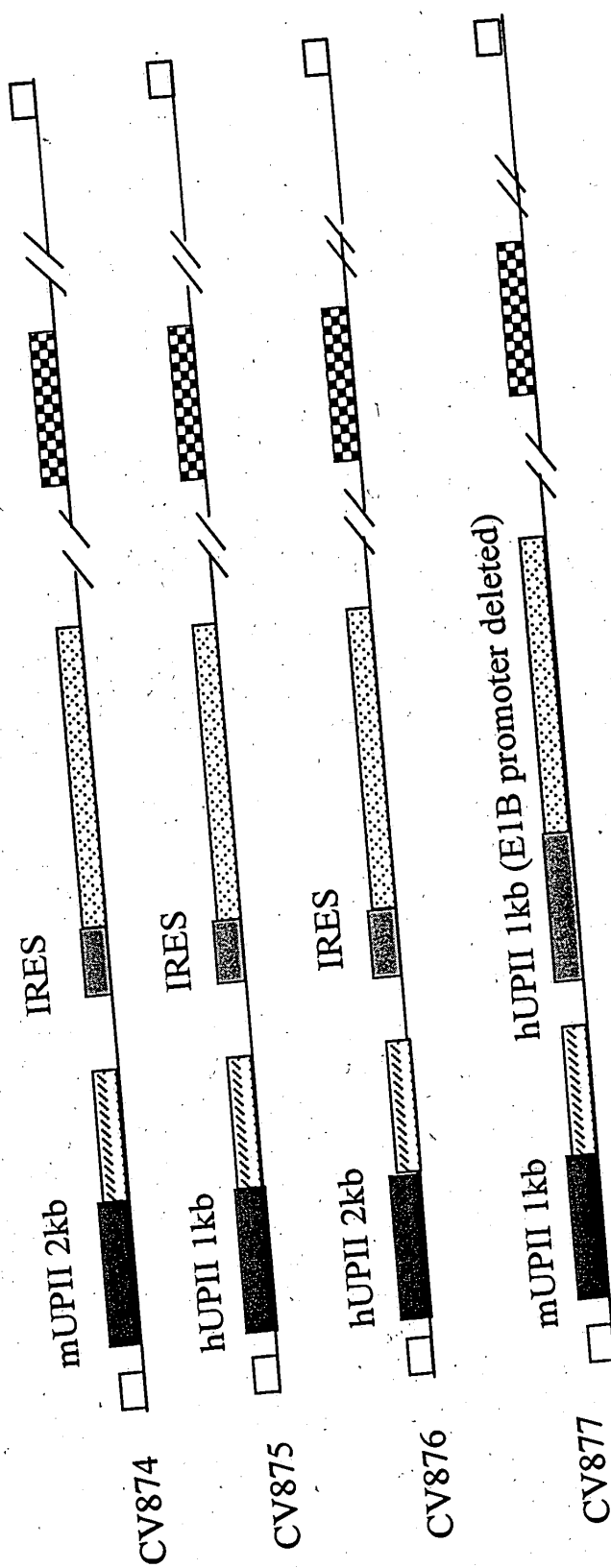
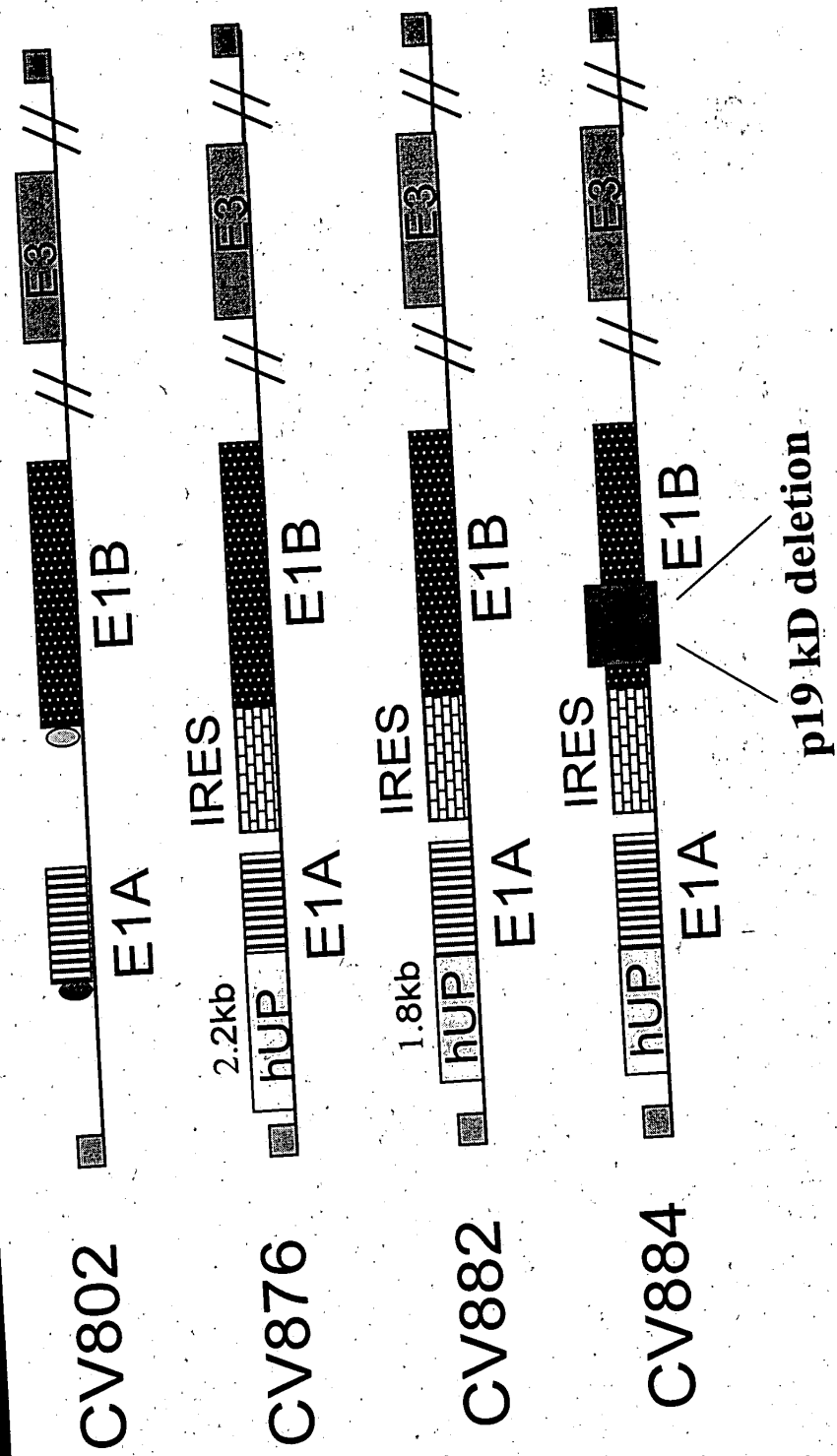




Figure 4G

# Structure of CV876, CV882 and CV884





# Bladder Specificity of Mouse/Human Uroplakin II promoters

## Luciferase Assay

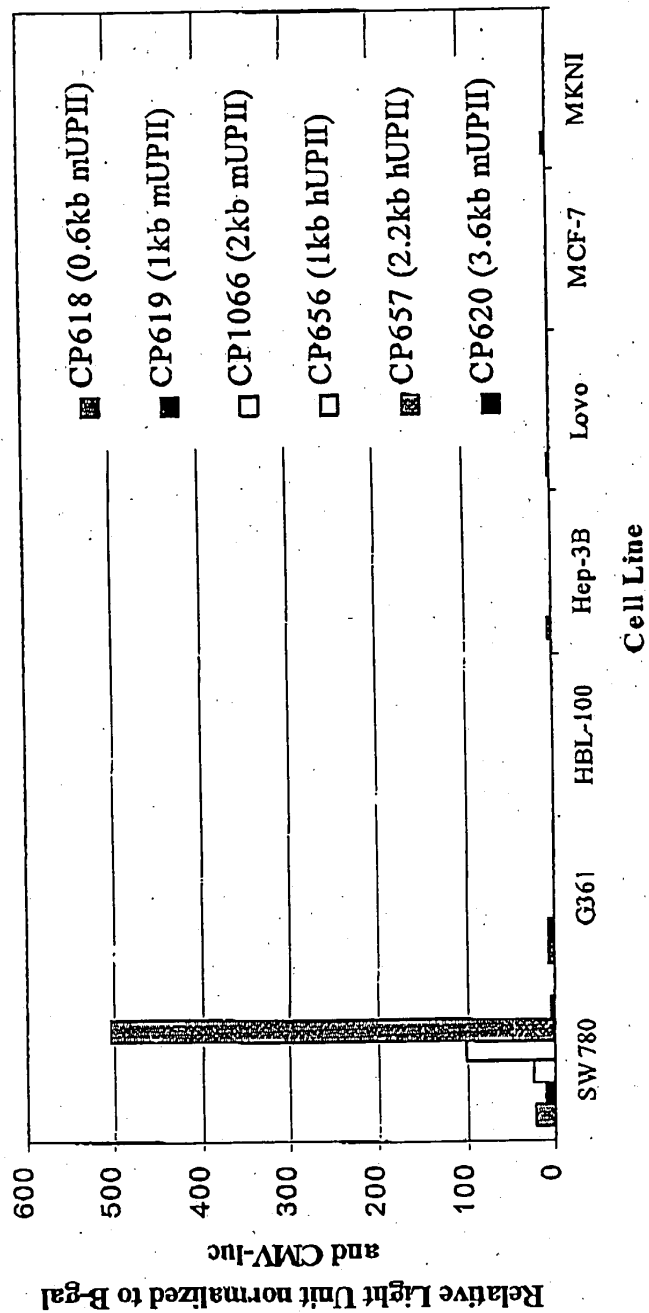


FIG. 7

FIG. 7

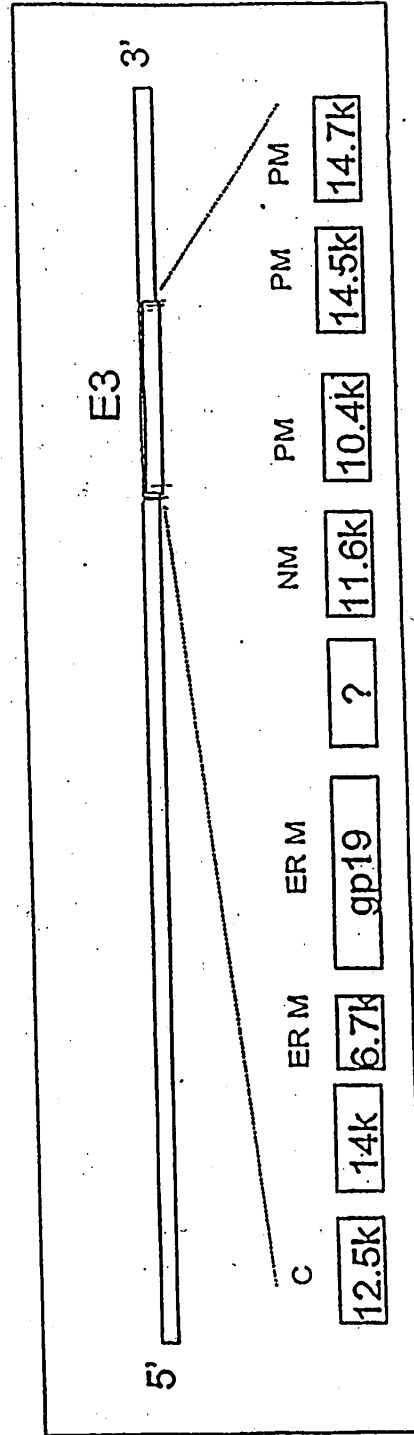


FIG. 8

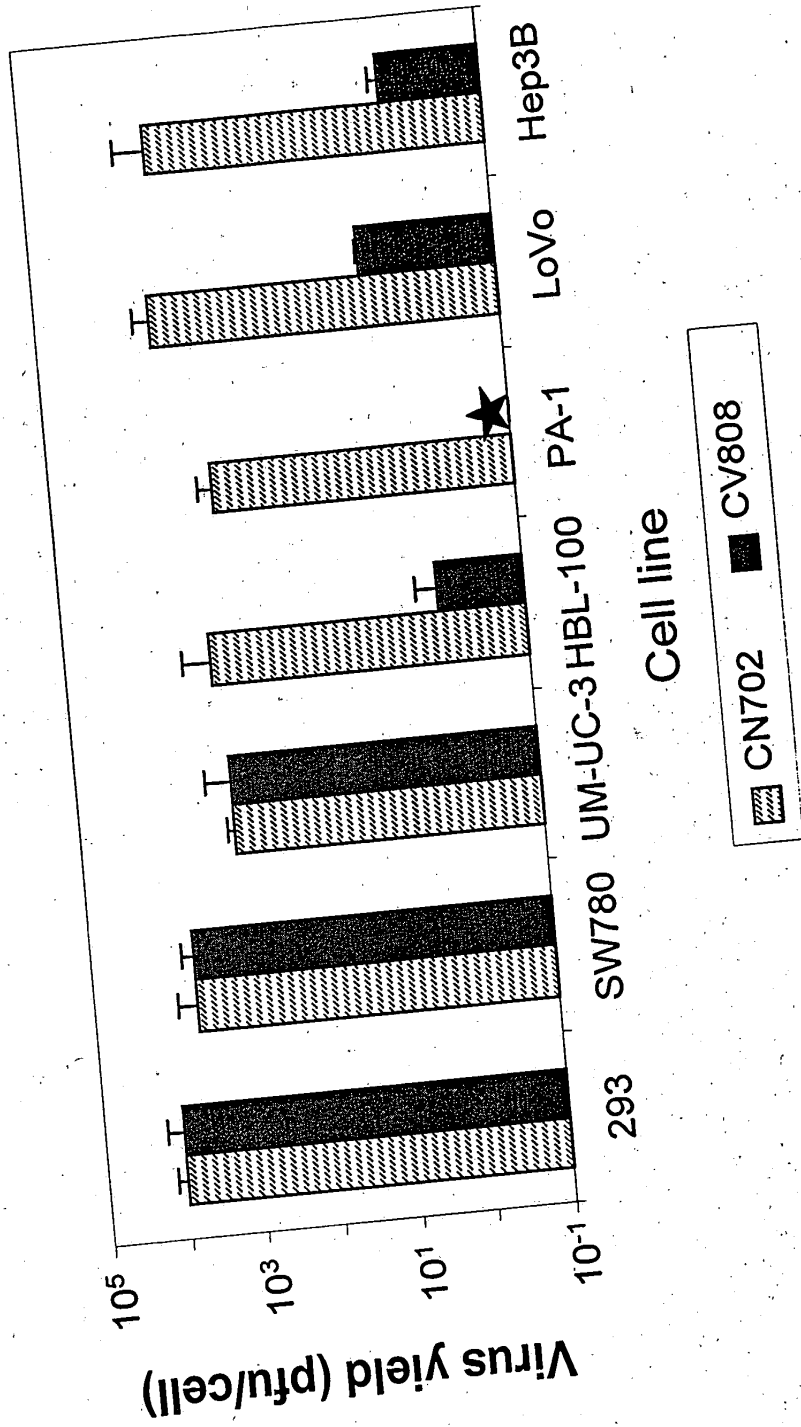
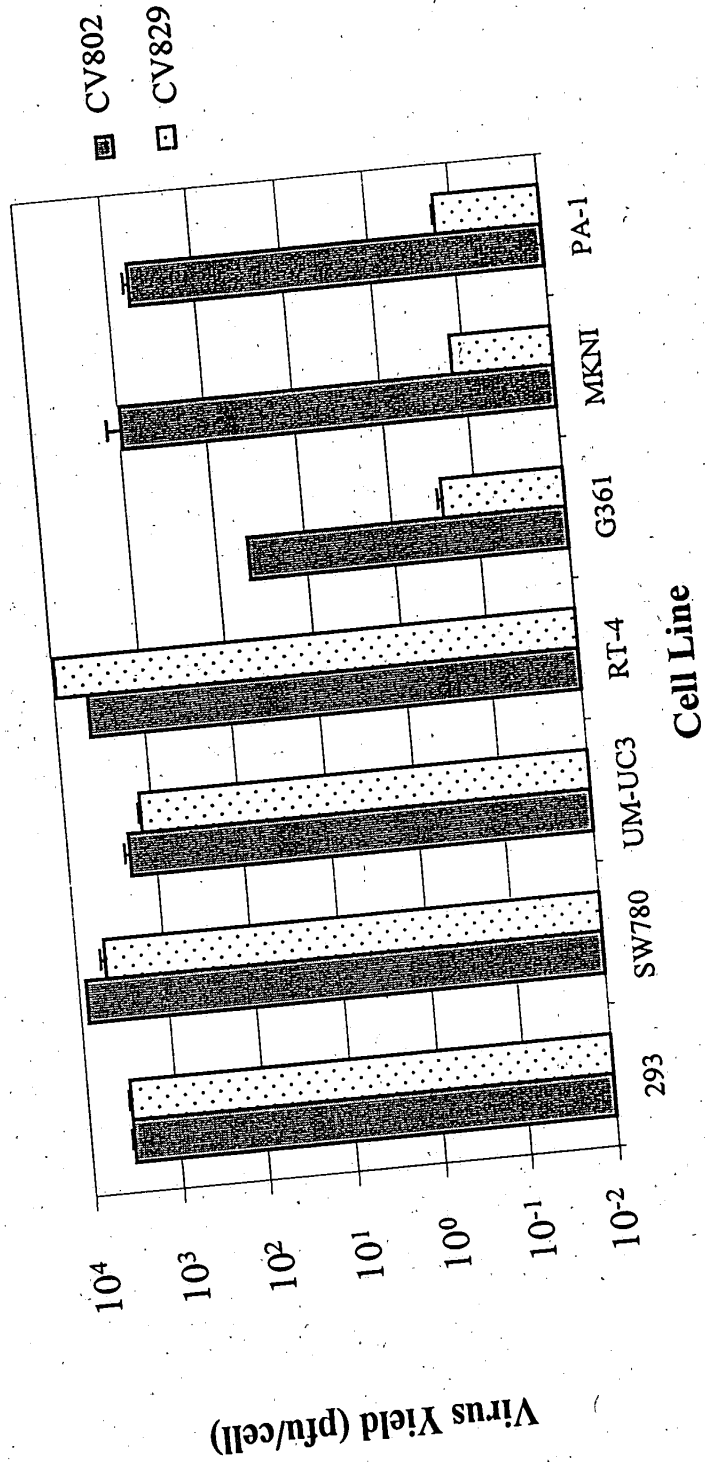
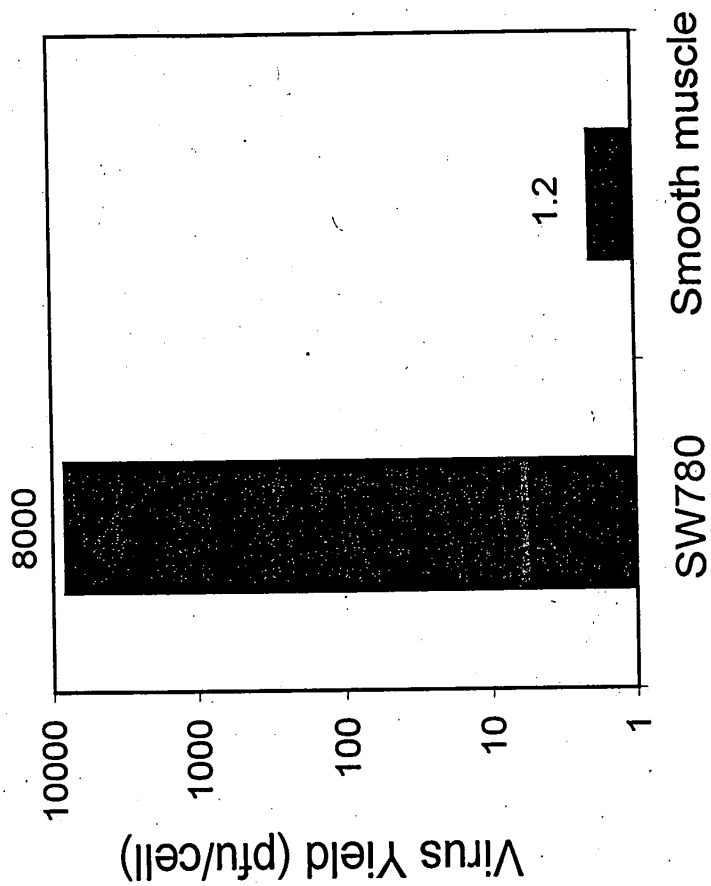


FIG. 9



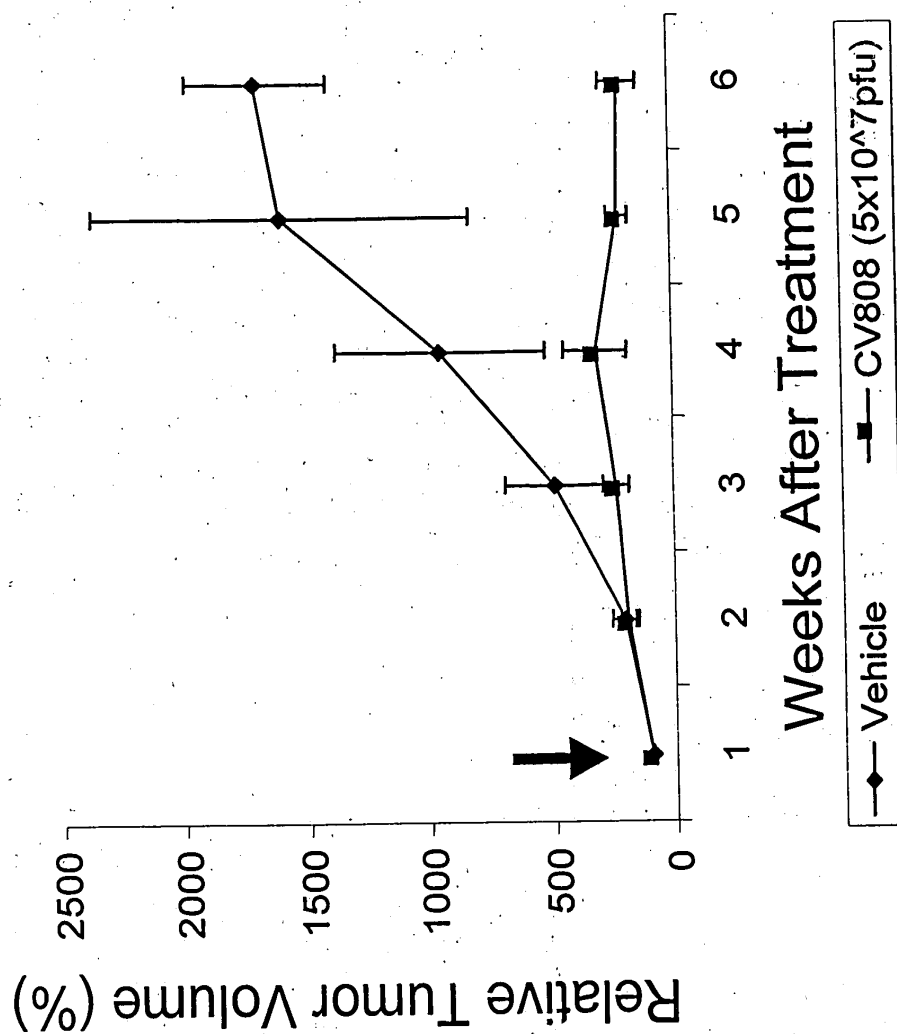
TOP SECRET

FIG. 10



TOPIC 2627360

FIG. 11





# FIG. 12

G ATG ACC GGC TCA ACC ATC GCG CCC ACA ACG GAC TAT CGC AAC ACC  
46

Met Thr Gly Ser Thr Ile Ala Pro Thr Thr Asp Tyr Arg Asn Thr  
1 5 10 15

ACT GCT ACC GGA CTA ACA TCT GCC CTA AAT TTA CCC CAA GTT CAT GCC  
94

Thr Ala Thr Gly Leu Thr Ser Ala Leu Asn Leu Pro Gln Val His Ala  
20 25 30

TTT GTC AAT GAC TGG GCG AGC TTG GAC ATG TGG TGG TTT TCC ATA GCG  
142

Phe Val Asn Asp Trp Ala Ser Leu Asp Met Trp Trp Phe Ser Ile Ala  
35 40 45

CTT ATG TTT GTT TGC CTT ATT ATT ATG TGG CTT ATT TGT TGC CTA AAG  
190

Leu Met Phe Val Cys Leu Ile Ile Met Trp Leu Ile Cys Cys Leu Lys  
50 55 60

CGC AGA CGC GCC AGA CCC CCC ATC TAT AGG CCT ATC ATT GTG CTC AAC  
238

Arg Arg Arg Ala Arg Pro Pro Ile Tyr Arg Pro Ile Ile Val Leu Asn  
65 70 75

CCA CAC AAT GAA AAA ATT CAT AGA TTG GAC GGT CTG AAA CCA TGT TCT  
286

Pro His Asn Glu Lys Ile His Arg Leu Asp Gly Leu Lys Pro Cys Ser  
80 85 90 95

CTT CTT TTA CAG TAT GAT TAA  
307

Leu Leu Leu Gln Tyr Asp  
100

00514200-03240

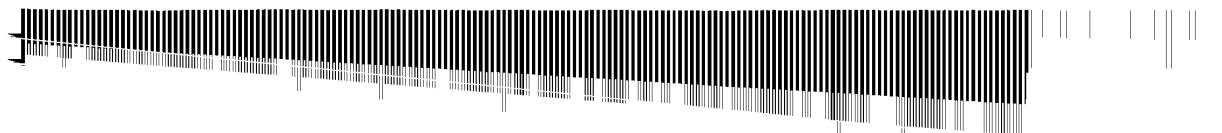


FIG. 13

# Region E3 of Adenovirus

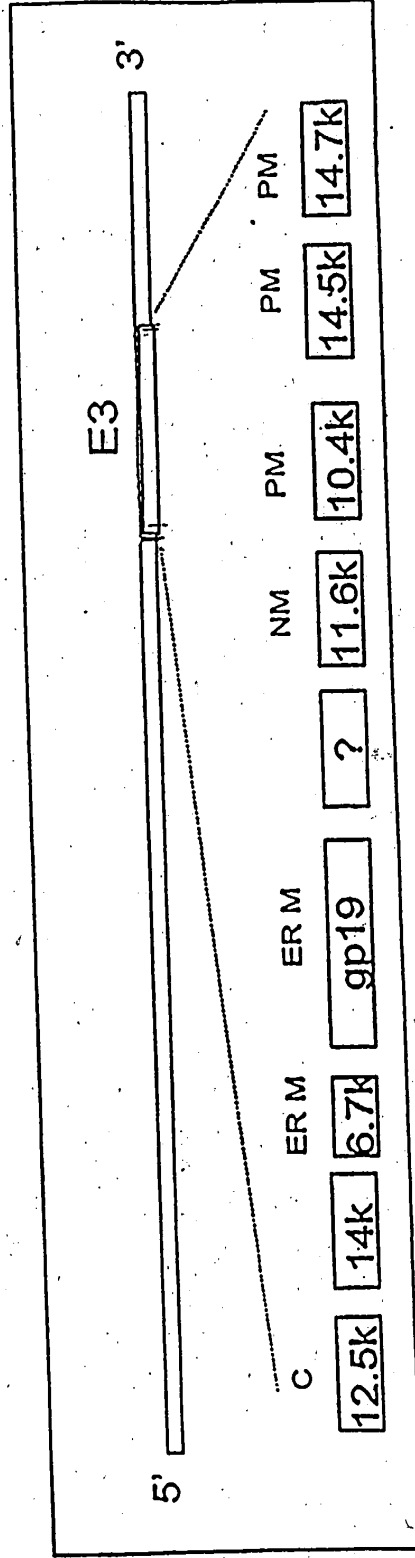


FIG. 14

# Virus Yield of CV884

